

Fig. 1

PPSS - I

SEQ ID NO: 8 5'GGGGGGGGGAACAGGAGCAGCAGAACTCAAAGAGAAGCCATCTCAACGATTGTCTGCCCAATTGAACCACCTTTATCC 81
ATCCTCTGCTCCCGAGACCCAGAGAAG ATG CTC TCG ACG CGT GTC CAG TGC GCC CTA GCA CTA CTC 152
Met Leu Ser Thr Arg Val Gln Cys Ala Leu Ala Leu Leu -88
SEQ ID NO: 3
TCC CTA GCC CTG GCC ATC AGC AGC GTC TCT GCC GCT CCG TCC GAT GCC AAA CTC CGC CAG CTG 214
Ser Leu Ala Leu Ala Ile Ser Ser Val Ser Ala Ala Pro Ser Asp Ala Lys Leu Arg Gln Leu -67
CTC CAA CGG TCA CTC ATG GCA CCT GCA GGC AAA CAG GAG CTT GCC AGG AAT ACA CTC GTA GAG 272
Leu Gln Arg Ser Leu Met Ala Pro Ala Gly Lys Gln Glu Leu Ala Arg Asn Thr Leu Val Glu -46
CTA CTC TCA GAG CTC GCA CAT GTA GAG AAC GAG GCG ATT GAA TTG GAT GAC ATG TCT CAT GGC 340
Leu Leu Ser Glu Leu Ala His Val Glu Asn Glu Ala Ile Glu Leu Asp Asp Met Ser His Gly -25
GTG GAG CAG GAG GAT GTG GAT CTC GAG CTG GAG CGT GCA CCC GGC CCA GTA CTG GCT CCA CGT 403
Val Glu Gln Glu Asp Val Asp Leu Glu Leu Glu Arg Ala Pro Gly Pro Val Leu Ala Pro Arg -4
GAA CGC AAG GCT GGA TGC AAG AAC TTC TTC TGG AAG ACC TTT ACA TCG TGT TAA TGAATCTACTC 466
Glu Arg Lys Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys ***
CTTACTGTGTACTACATCTCATCTCTTTTGTTCATCACTCATTTGCTGAATCCAATGCACCATGGCCTAACCCCTCTCT 549
TCAAAAAATTTAAATAAACACTGTTATACCTTTAACAATCATTTCTGATGTTTCTATCGCTCACTTAGATTTTTTCCGAAAAG 632
GAACACAAGAAAGATGTTCTACAAATGTATGCGTTCTGCTTGACTGTGATTATGTATTTGGCAGACTATTTTAAATTG 715
TTTGTGTTGATATAATCTGTGTTTCAGAACCAAAAAAAAAAAAAA 3'

Fig. 2

PPSS-II' and PPSS-II''

SEQ ID NO: 14 PPSS-II' accaggcctgctccataaccgactgacccagatcgagcagatagcccggtccagctcagctcgtctccacccggtgcc 75
 SEQ ID NO: 20 PPSS-II'' accaggcctgctccataatcaactgatctagatccagcaccaccccggtccagcttagctc*****acggtgctcgg 70

SEQ ID NO: 9 Lys Cys Arg
 PPSS-II' tccctgcaaaccaaacccagctctgttggag ATG AAG GTC TGC CGA ATC CAC TGT GCC CTG GCC 139/-91
 PPSS-II'' tccctgcaaacccaaactcagctctgttggag ATG AGG GTC TCC CAA ATC CAC TGT GCA CTG GCC 134/-87

SEQ ID NO: 15 Met Arg Val Ser Gln Ile His Cys Ala Leu Ala
 PPSS-II' CTG CTG GGT TTG GCC CTG GCC ATT TGC AGC CAA GGA GCC GCC TCG CAG CCC GAC CTG 196/-72
 PPSS-II'' CTG CTG GGT CTG GCC CTG GCA ATT TGC AGC CAA GGA GCC GCC TCG CAG CCA GAC CTG 191/-68
 Leu Leu Gly Leu Ala Leu Ala Ile Cys Ser Gln Gly Ala Ala Ser Gln Pro Asp Leu

Arg Arg
 PPSS-II' GAC CTC CGC AGC CGC AGA CTC CTT CAG AGG GCT CGT GCC GCT GCA TTG CCA CAC AGG 253/-53
 PPSS-II'' GAC CTC GCG AGC CGC CGA CTC CTC CAG AGG GCC CTG GCC GCT GCA TTG CCA CAC AGG 248/-49
 Asp Leu Ala Ser Arg Arg Leu Leu Gln Arg Ala Leu Ala Ala Leu Pro His Arg

PPSS-II' AGT GGA GTA AGC GAG CCG TGG AGG ACA TTC TAT CCC AAC TGT CCT TGC CTG *** ** 304/-35
 PPSS-II'' AGT GGA GTA AGC GAG CGA TGG AGG ACA TTC TAT CCG AAC TGT CCT TGC CTG AGG TGG 305/-30
 Ser Gly Val Ser Glu Arg Trp Arg Thr Phe Tyr Pro Asn Cys Pro Cys Leu Arg Trp

Cys Ala Gly Leu Arg Val Glu
 PPSS-II' AGG CCC AGG AAA GTG AAG TGT CAA *** GCG GGG GCT AAA GAG GAC CTG CGT GTG GAG 358/-18
 PPSS-II'' AGG CCC AGA AAA GTG AAG GGT CCA CAG CTG AAG GCC AAA GAG GAC *** ** 350/-14
 Arg Pro Arg Lys Val Lys Gly Pro Gln Leu Lys Ala Lys Glu Asp

Gly Asn Pro Asn
 PPSS-II' CTG GAG CGC TCA GTG GGC AAC CCC AAC AAC CTT CCC CCC CGT GAG CGC AAA GCC GGC 415/+2
 PPSS-II'' CTG GAG CGC TCA GTG GAC *** ** AAC CTT CCC CCC CGC GAG CGC AAA GCT GGC 398/+2
 Leu Glu Arg Ser Val Asp Asn Leu Pro Pro Arg Glu Arg Lys Ala Gly

PPSS-II' TGC AAG AAC TTC TAC TGG AAG GGC TTC ACT TCC TGC tga ggaagaataaacgaccacctt 477
 PPSS-II'' TGC AAG AAC TTC TAC TGG AAG GGA TTC ACT TCT TGC taa ggaagaaaagcctgaccacctt 460
 Cys Lys Asn Phe Tyr Trp Lys Gly Phe Thr Ser Cys ###

PPSS-II' atgacatgacgctgccaatcacgtcacaccgccaacttaacacctgacgaatgcagccaatcaacagtttagctgtg 552
 PPSS-II'' atgacacaatgcattcaatcacatcacaccgccaacttcattctgactaatgtagccaatcagcaatttagctgtg 535

PPSS-II' cccgatgatgggttcttgaatcaacagaatgatgtacctgtctaatattgtgaaataaataataaataaattg(a)n
 PPSS-II'' cctgatgacaattatgattatgatgtacctgactaatttagaataaagagaaataaagagaaac(a)n

Fig. 3

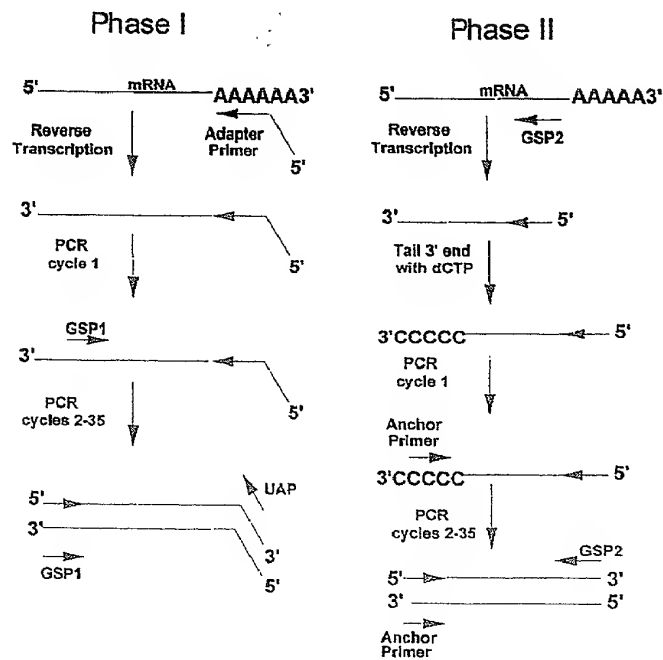


Fig. 4

Nucleotide Identity

| | | | | | | | | | | |
|--------|--------|------|------|------|------|------|------|------|------|------|
| TR II' | 82.8 | 49.0 | 43.7 | 52.3 | 51.0 | 52.0 | 51.5 | 51.1 | 52.8 | 54.5 |
| 84.1 | TR II' | 48.2 | 39.1 | 44.9 | 50.0 | 50.0 | 49.5 | 48.0 | 49.8 | 52.5 |
| 45.5 | 43.9 | TRI | 58.1 | 77.0 | 67.7 | 68.9 | 67.9 | 69.4 | 69.4 | 72.5 |
| 35.6 | 35.6 | 52.3 | AFI | 60.1 | 58.8 | 55.1 | 53.8 | 55.3 | 56.8 | 56.8 |
| 44.7 | 40.9 | 73.5 | 52.3 | CFI | 65.7 | 68.7 | 67.7 | 68.4 | 67.7 | 72.2 |
| 47.7 | 44.7 | 70.5 | 49.2 | 64.4 | FR I | 75.0 | 74.5 | 62.6 | 75.5 | 78.3 |
| 42.4 | 38.6 | 66.7 | 46.2 | 63.6 | 78.8 | C | 84.1 | 84.3 | 84.3 | 84.3 |
| 42.4 | 38.6 | 65.2 | 45.5 | 62.9 | 78.0 | 87.9 | R | 92.4 | 91.2 | 92.2 |
| 42.4 | 38.6 | 66.7 | 46.2 | 63.6 | 78.8 | 88.6 | 97.0 | B | 94.4 | 95.5 |
| 42.4 | 38.6 | 64.4 | 46.2 | 62.9 | 78.8 | 90.9 | 96.2 | 98.5 | M | 98.7 |
| 45.5 | 42.4 | 73.5 | 47.7 | 68.2 | 87.1 | 91.7 | 97.7 | 98.5 | 100 | H |

Amino Acid Identity

Fig. 5

Fig. 6

Comparison of Amino Acid Sequences of Peptides Derived from Preprosomatostatin 1^a

| | -20 | -10 | +1 | +10 | +14 | | | | | |
|----------------------------|-----|-----------|-----------|-------|--------|--------|----------|-----------|-----------|-----------|
| Rainbow trout ^b | | | | | | | | | | |
| Hagfish ^d | | APG**PVLA | PRERK | AGCKN | FFWKTF | TSCSEQ | ID NO: 4 | | | |
| Lamprey ^d | | AVERP | RQDGV | HEP | PGRERK | AGCKN | FFWKTF | TSCSEQ | ID NO: 27 | |
| Torpedo ^d | | | | | | AGCKN | FFWKTF | TSCSEQ | ID NO: 1 | |
| Ratfish ^d | | | | | | AGCKN | FFWKTF | TSCSEQ | ID NO: 1 | |
| Bowfin ^d | | | | | | AGCKS | FFWKTF | TSCSEQ | ID NO: 28 | |
| Sturgeon ^d | | | SAN**PALA | PRERK | AGCKN | FFWKTF | TSCSEQ | ID NO: 29 | | |
| Catfish ^d | | | | | | APCKN | FFWKTF | TSCSEQ | ID NO: 30 | |
| Salmon ^d | | | | | | AGCKN | FFWKTF | TSCSEQ | ID NO: 1 | |
| Anglerfish ^c | | | | | | AGCKN | FFWKTF | TSCSEQ | ID NO: 1 | |
| Eel ^d | | | ASGGP | LLA | PRERK | AGCKN | FFWKTF | TSCSEQ | ID NO: 31 | |
| Flounder ^d | | | | | | AGCKN | FFWKTF | TSCSEQ | ID NO: 1 | |
| Sculpin ^d | | | | | | AGCKN | FYWKGF | TSCSEQ | ID NO: 2 | |
| Frog ^c | | | | | | AGCKN | FYWKGF | TSCSEQ | ID NO: 2 | |
| Salamander ^d | | | | | | AGCKN | FFWKTF | TSCSEQ | ID NO: 1 | |
| Alligator ^d | | | | | | AGCKN | FFWKTF | TSCSEQ | ID NO: 1 | |
| Pigeon ^d | | | | | | AGCKN | FFWKTF | TSCSEQ | ID NO: 1 | |
| Ovine ^d | | | SAN | SNP | AMA | PRERK | AGCKN | FFWKTF | TSCSEQ | ID NO: 32 |

SEQUENCE COMPARISON

| | | | |
|---------------|--------|---|-----------------------------|
| SEQ ID NO: 9 | TRII' | ---MKVCRTHCALATLGLALATCSQGAASQP----- | DLDLRSRRLLORARAAWPHRSQVSEK |
| SEQ ID NO: 15 | TRII'' | ---MRYSQTHCALATLGLALATCSQGAASQP----- | DLDTASRRLLORALAAALPHRSQVSEK |
| SEQ ID NO: 36 | CFII | ---MSSSPLRLALATMCLVSAVGVISCGRP----- | HVVLSNADEEARNVPFGEEVPERLT |
| SEQ ID NO: 37 | AFII | ---MQCTRCPAIHALATVLCGPSVSSQLDREQSDNQDLDLELRQHWITERRASAGLLSQEWSKRA | DI DFRHHRLERASATGOATQDFTKRD |
| SEQ ID NO: 38 | GFII | ---MRLCELHCYATLGLGTSVLCGRCAASQL--EP-- | PVEERNPAOSRELSKE-RKELILKL |
| SEQ ID NO: 39 | GFIII | ---MQLSSIVSLVLYSVRAAVL----- | PDDNRITTGRIQNQLNAIQDLLLLKL |
| SEQ ID NO: 40 | FRII | ---MLGSAGTILLLLAW-GARALSO----- | DAKLROLLORSIMAPAGKQELARNT |
| SEQ ID NO: 3 | TRI | ---MLSTRVQCALATLSLALATSSVSAAPS----- | DAKLROFLQRSILAPSVKQELTRYT |
| SEQ ID NO: 41 | CFI | ---MPSTRIOCALATLCAVALSVCSVSGAPS----- | DSKLRLLEHRYPLQCS-KQDMTRSA |
| SEQ ID NO: 42 | AFI | MKMVSSSRLRCLLVLLSLTASISCSFAGQR----- | DAKLROLLORSLLNPAGKQELARYT |
| SEQ ID NO: 43 | GFI | ---MLSTRIOCALATLSLALAVCSVSAAPT----- | DPRLRQFLQKSLASAG-KQELAKYF |
| SEQ ID NO: 44 | FRI | ---MOSERVQCAITLISLALAINSISAAPT----- | DPRLRQFLQKSLAAAGKQELAKYF |
| SEQ ID NO: 45 | C | ---MLSCRLOCALATLSLALAVGTVSAAPS----- | DPRLRQFLQKSLAAAGKQELAKYF |
| SEQ ID NO: 46 | R | ---MLSCRLOCALAALCIVLALGGVTGAPS----- | DPRLRQFLQKSLAAAGKQELAKYF |
| SEQ ID NO: 47 | B | ---MLSCRLOCALAALSIIVLALGCVTGAPS----- | DPRLRQFLQKSLAAAGKQELAKYF |
| SEQ ID NO: 48 | M | ---MLSCRLOCALAALSIIVLALGCVTGAPS----- | DPRLRQFLQKSLAAAGKQELAKYF |
| SEQ ID NO: 49 | H | ---MLSCRLOCALAALSIIVLALGCVTGAPS----- | DPRLRQFLQKSLAAAGKQELAKYF |

(continued)

WRTEVPNCPCLR--ERKVKCP-AGAKE-DLR--VELERSVGN-PNNLP PRERKAGCKNFWYKGETSC
 WRTEVPNCPCLRWRPRKVKGPQIAKAKE-DL-----ERSV---DNLP PRERKAGCKNFWYKGETSC
 LPELOW-MLSNNELT PVQVEEAPRS-----RLELVRRDN-----T-VTSKPLNEMNYFWKSRATC
 VEELLAQMSLPEATFORFAEDASHATE-G---RMNLEERSVDS-TNNLP PRERKAGCKNFWYKGETSC
 VEKLLSLLSIPEMEMR--EKGLSMAGE-SEDLRLLEOERSAES-SNOLETRVRKEGCKNFWYKGETSC
 ISGLLD--GVDNSVLDGEIAPVPFDAEEPLESRLE-ERAVYNRLSOLPQRDKAPCKNEFWKTEFSC
 LSGWTD--S-RESNLVEVERNVPDPPE-P-----KIPPSVK--FPRISLERKAPCKNEFWKTEFMC
 LVELLS-FLAHVENEAEILODMSHGVE-QEDVLELERAPG--PVLA PRERKAGCKNFWKTEFSC
 LAELLA-ELAEAENEVLDSDEVSPAAE-SEGARLEMERAAE---PMIAP PRERKAGCKNFWKTEFSC
 LAELIISDOLLOGENEALEENFPLAEGGPEDAHADLERAASG-GPLA PRERKAGCKNFWKTEFSC
 LAOLLS-ELVOAENEALEPEDLSRAVE-KDEVRLERLERAAG--PMIAP PRERKAGCKNFWKTEFSC
 LAELIS-EPSTQDNEALESDDLPRGAE-QDEVRLERLERSANS-SPALAP PRERKAGCKNFWKTEFSC
 LAELIS-EPSTQDNEALESDDLPRGAE-QDEVRLERLERSANS-NPALAP PRERKAGCKNFWKTEFSC
 LAELLS-EPNQTENDALEPEDLPQAAE-QDEMRLERLORSANS-NPAMAP PRERKAGCKNFWKTEFSC
 LAELLS-EPNQTENDALEPEDLSQAAE-QDEMRLERLORSANS-NPAMAP PRERKAGCKNFWKTEFSC
 LAELLS-EPNQTENDALEPEDLSQAAE-QDEMRLERLORSANS-NPAMAP PRERKAGCKNFWKTEFSC
 LAELLS-EPNQTENDALEPEDLSQAAE-QDEMRLERLORSANS-NPAMAP PRERKAGCKNFWKTEFSC

Fig. 7

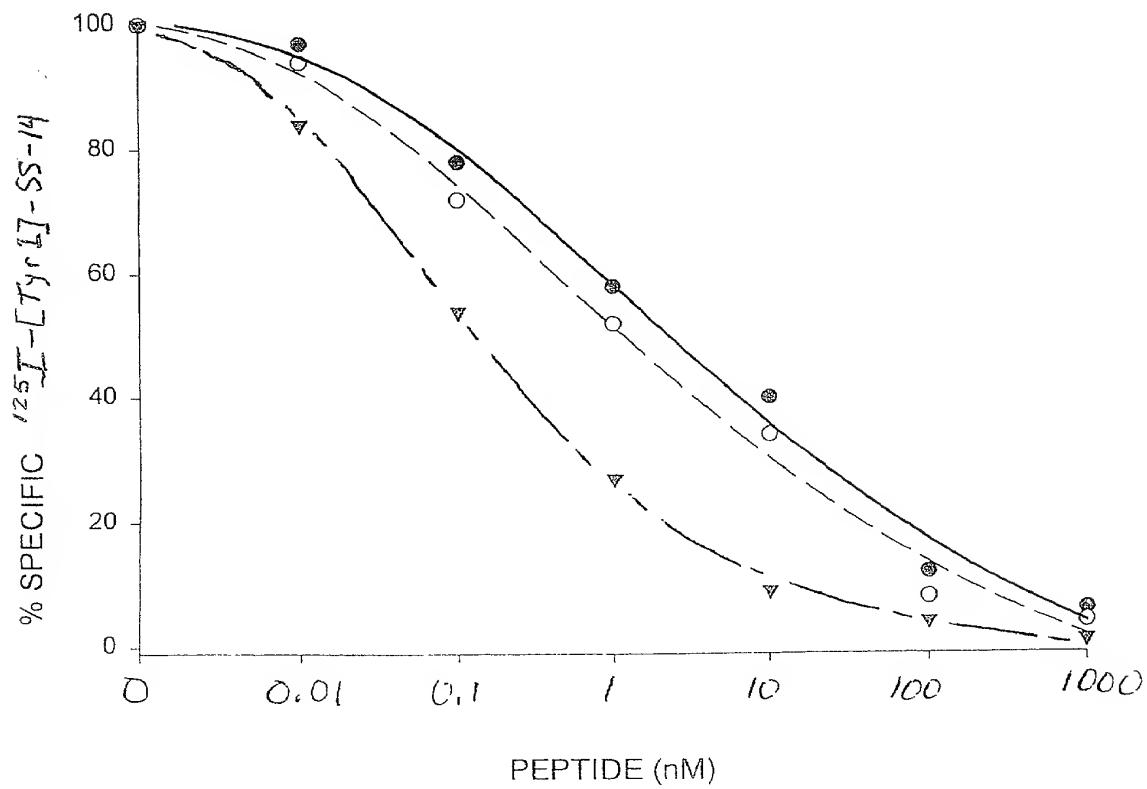


Fig. 8